# Bacterial wilt resistance in tomato, eggplant and pepper: genetic resources challenged with the multifaceted *Ralstonia solanacearum* species complex

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Bacterial wilt caused by strains belonging to the *Ralstonia solanacearum* species complex inflicts severe economic losses in many crops worldwide. Host resistance remains the most effective control strategy against the bacterial wilt. However, interactions among plant, strain and environment often result in overcoming resistance properties due to variation in strain pathogenicity and adaptation. To help breeders circumvent this problem, we assembled a worldwide collection of 30 accessions of Tomato, Eggplant and Pepper (Core-TEP) that are commonly used as sources of resistance to *R. solanacearum* or for mapping QTLs. The Core-TEP lines were challenged with a core collection of 12 pathogen strains (Core-Rs2) representing the phylogenetic diversity of *R. solanacearum*. To our knowledge, this is the first study that investigated bacterial wilt resistance in a set of worldwide genetic resources used as sources of resistance in three solanaceous species (tomato, eggplant, and pepper). Our results showed that none of the Core-TEP accessions, representative of the TEP genetic diversity for resistance, was resistant to all Core-Rs2 strains. Hence, none of them displayed universal resistance. We observed six wilt interaction phenotypes, from highly susceptible to highly resistant. Intermediate phenotype resulted from the ability of plants to tolerate latent infections, i.e. bacterial colonization of vascular elements with limited or no wilting. *R. solanacearum* strains exhibited specific patterns of interaction with Core-TEP accessions. Thanks to several similarities of virulence patterns between strains of Core-Rs2, we defined two working concepts associated with two levels of resolution of the interactions between strains and plant phenotypes. One concept, the "pathoprofile" is based on the interactions for the three solanaceae taken together, and the other, the pathotype is based on the interactions for each plant species taken separately. The 12 Core-Rs2 strains partitioned into four pathotypes on Pepper accessions, five pathotypes on Tomato, six pathotypes on Eggplant, and six pathoprofiles on the whole set of Core-TEP accessions. Neither pathotypes nor pathoprofiles were phylotype-specific. Pathoprofiles with high pathogenicity were mainly found in strains from phylotypes I, IIB and III. One pathoprofile included a strain that overcame almost all resistance sources.

**Keywords:**
*Ralstonia solanacearum*, resistance, *Solanaceae*, pathotype, pathoprofile